From: Praskins, Wayne [/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP
(FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=4F47BC0A2C2E42A98347D59CD1A98B19-WPRASKIN]
Sent: 1/28/2021 11:56:33 PM
To: Hays, David C Jr CIV USARMY CENWK (USA) [David.C.Hays@usace.army.mil]
Subject: RE: HPNS: Navy swipe sample results

Dave –

I'm thinking about your idea of accounting for alpha-emitting progeny when comparing gross alpha measurements to BPRGs. Does the following capture (and extend) our discussion?

- I'm pretty sure that the BPRGs for the alpha emitting HPNS radionuclides assume secular equilibrium of all progeny (and no radon loss). (Looked at user's guide and talked with Stuart.) If this assumption is maintained, as you explain in your email, a 20 dpm gross alpha measurement would represent 4 dpm Ra-226
- Similarly, a 20 dpm gross alpha measurement would represent about 3 dpm Th-232 (5 alpha emitting progeny), U-235 (6 progeny), and Pu-239 (7 progeny)
- No such adjustment for Am-241 since it has no alpha emitting progeny
- Conversely, the MDA required to achieve the BPRGs would be:

	A	B	
	BPRG (dpm/100cm2)	Parent + Alpha-emitting progeny	Gross alpha MDA to achieve BPRG, assuming 100% equilibrium btwn Rn and progeny
Am-241	4.4	1 + 0	4.4
Pu-239	4.1	1 + 7	33
Ra-226	1.2	1 + 4	6
Th-232	2.4	1 + 5	14
U-235	4.7	1 + 6	33

- So, if 100% equilibrium is assumed, and Am-241 could be present, you would want the gross alpha MDA to be at or less than 4.4?
- At most of the Hunters Point buildings, Am-241 is not listed as a radionuclide of concern. We would need to decide if it's appropriate to assume that radionuclides not identified as radionuclides of concern are not present.
- If 50% equilibrium were assumed between radon and its progeny, how would you calculate the MDA? For Ra-226, would you multiply by 3, to reflect the parent and four progeny at half the parent's activity (1 + 4 * ½ = 3)?
- Do you know of site examples where an equilibrium value less than 100% has been used? Would the value vary between radionuclides, depending on the radon isotope in the decay chain? In their HPNS RESRAD BUILD simulations, the Navy assumed 10% loss (i.e., progeny remain at 90% of the radon parent concentration).

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From: Hays, David C Jr CIV USARMY CENWK (USA) <David.C.Hays@usace.army.mil>
Sent: Wednesday, January 27, 2021 6:36 AM
To: Praskins, Wayne <Praskins.Wayne@epa.gov>
Subject: RE: HPNS: Navy swipe sample results

Wayne, yes. I may be driving all day today but regardless could take a call. I can make time on other days. When would be best for you this week? I concur with their statements of uncertainty with wipe testing.

FYI: The attached goes into deep detail about wipe sampling, and is likely too much info but FYI. Supports Navy declarations. Note: It fails to describe or present a path to converting gross counting activity to isotopic specific activity but please see below.

FYI: I looked at the attachments, data looks good for a 1 minute count. Note for estimating purposes; doubling the count time typically reduces the MDC by a factor of 1.4142 (i.e. the square root of 2). So a 2 min count should reduce alpha MDC to 11 dpm. I do think the Navy should also consider the specific isotope limit versus the non isotope specific counting approach. E.g. A gross alpha result of 20 dpm would need to be corrected to the specific isotope activity (Ra-226). Thus given the number of alpha decays assumed for the Ra-226 decay chain (accounting for Rn daughter equilibrium) the Ra-226 activity represented by a net gross alpha count of 20 dpm may be 20 dpm Ra-226 (assumes no equilibrium) to 4 dpm Ra-226 (assumes full equilibrium). Likely value is somewhere in between but they would have to defend their assumptions on that. This approach could be applied to estimating the Ra-226 MDC as well, but again Navy would need to make assumptions and defend them.